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Supplemental Information

Counteracting Activities of OCT4 and KLF4 during Reprogramming to Pluripotency

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Supplemental Data

Figure S1 related to Figure 1

Figure S2 related to Figure 3

Figure S3 related to Figure 3

Figure S4 related to Figure 6

Figure S5 related to Figure 6

Figure S6 related to Figure 6

Figure S7 related to Figure 6

Table S1 related to Figure 3

Table S2 related to Figure 3

Table S3 related to Figure 3

Table S4 related to Figure 3

Table S5 related to Figures 1, 2, 5, 6, 7, S5, and S6

Table S6 related to Figures 1, 2, and 7

Supplemental References

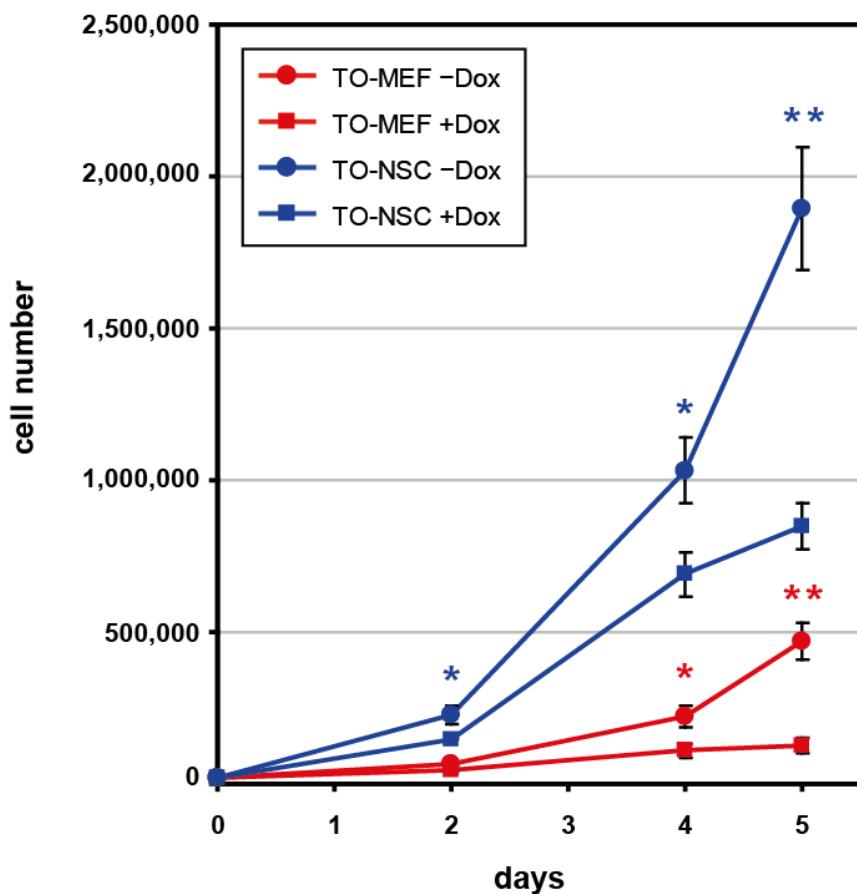


Figure S1, related to Figure 1. *Oct4* overexpression impairs the proliferation of MEFs and NSCs

20,000 cells were seeded on day 0, and *Oct4* was induced by doxycycline treatment from day 1 onwards. Error bars correspond to the standard error of the mean (biological replicates, $n = 4$). Asterisks indicate the probability of a true null hypothesis according to a two-tailed, unpaired Student's t-test: *, $p < 0.05$; **, $p < 0.005$.

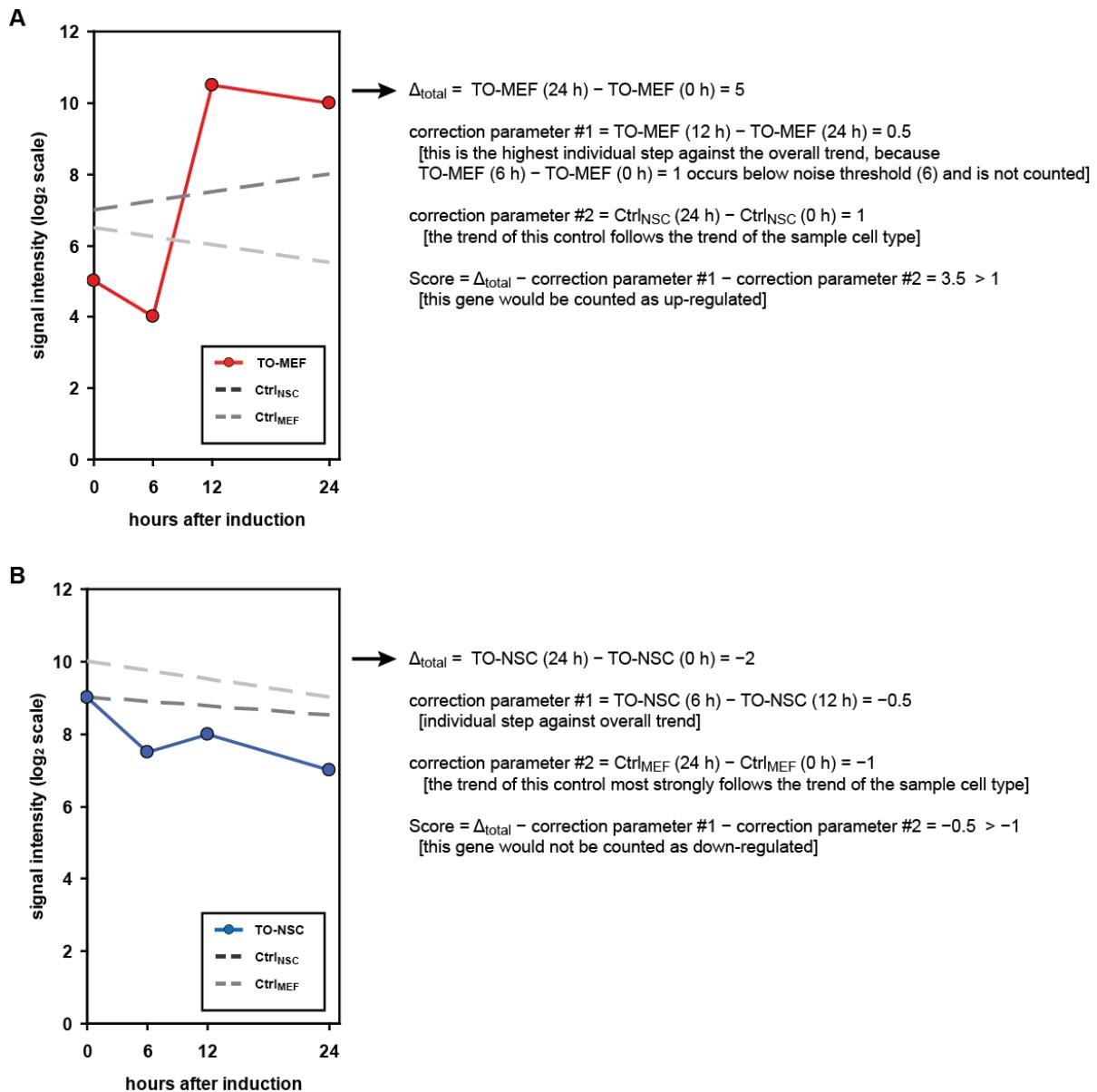


Figure S2, related to Figure 3. Examples to illustrate score calculation

(A) Example of progression in gene expression that fulfills the defined criteria for upregulation. (B) Example of progression in gene expression that does not fulfill the criteria for downregulation.

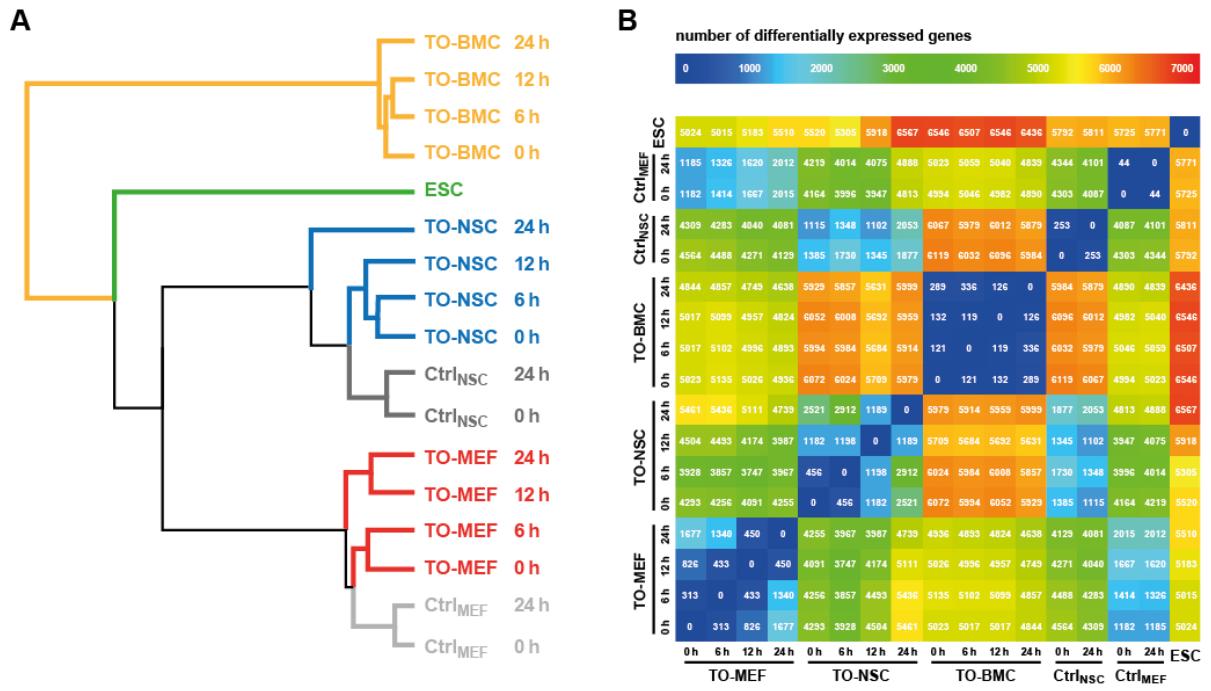


Figure S3, related to Figure 3. Comparative transcriptome analysis of *Oct4*-induced somatic cells and controls

(A) Dendrogram displaying the results of an unsupervised hierarchical clustering based on the correlation of global gene expression profiles. (B) Direct comparison of individual samples. The number of differentially expressed genes (≥ 2 -fold difference and signal ≥ 6 in at least one of the corresponding samples) is shown for each pair of samples and highlighted in shaded colors.

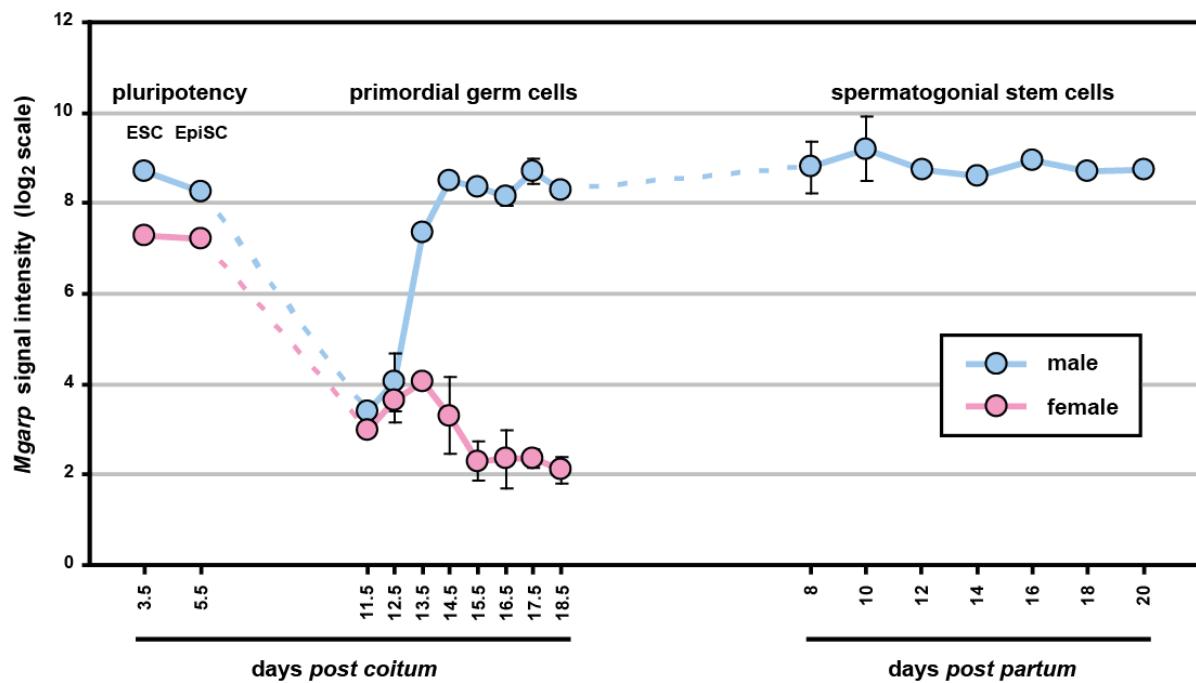


Figure S4, related to Figure 6. Expression of *Mgarp* mRNA in cells of the germline lineage at different developmental stages

The displayed data have been extracted from a microarray dataset previously published by our group (Sabour et al., 2011). Error bars correspond to the standard deviation of the mean (biological replicates, n = 2). EpiSC, epiblast stem cells.

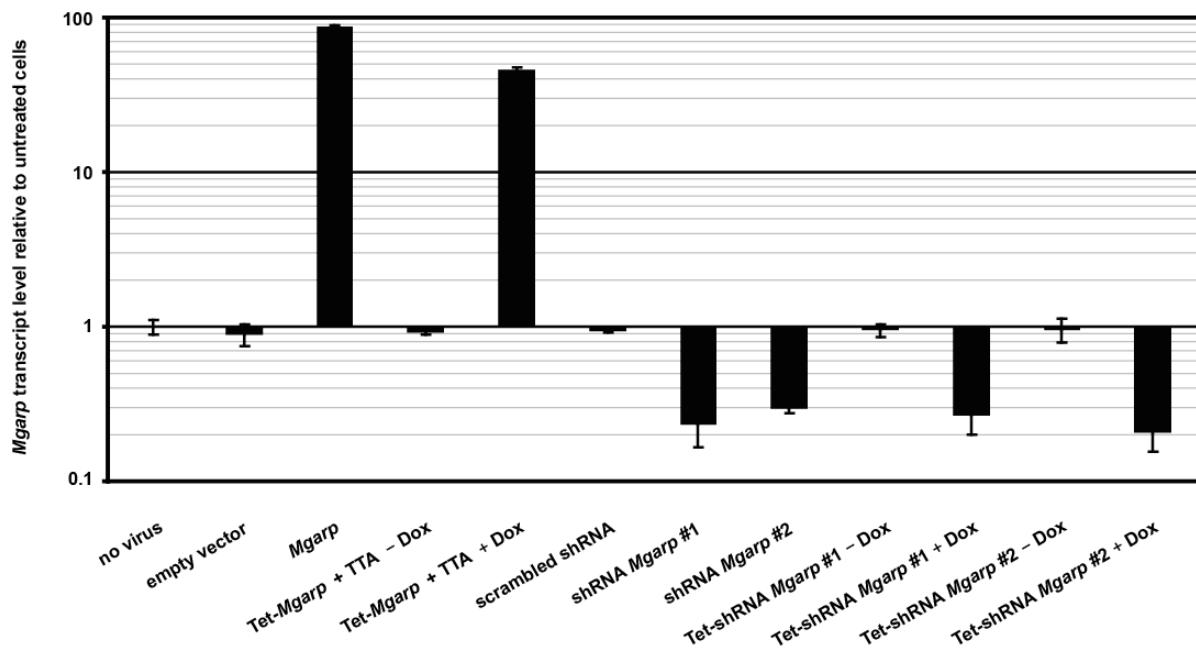


Figure S5, related to Figure 6. Validation of viral *Mgarp* overexpression and sh*Mgarp* knockdown constructs

qRT-PCR for *Mgarp* mRNA in MEFs 3 days after infection with the different viral vectors. Error bars correspond to the standard deviation of the mean (technical replicates, n = 3). Tet-, tetracycline-inducible; TTA, tetracycline transactivator. See also Table S5.

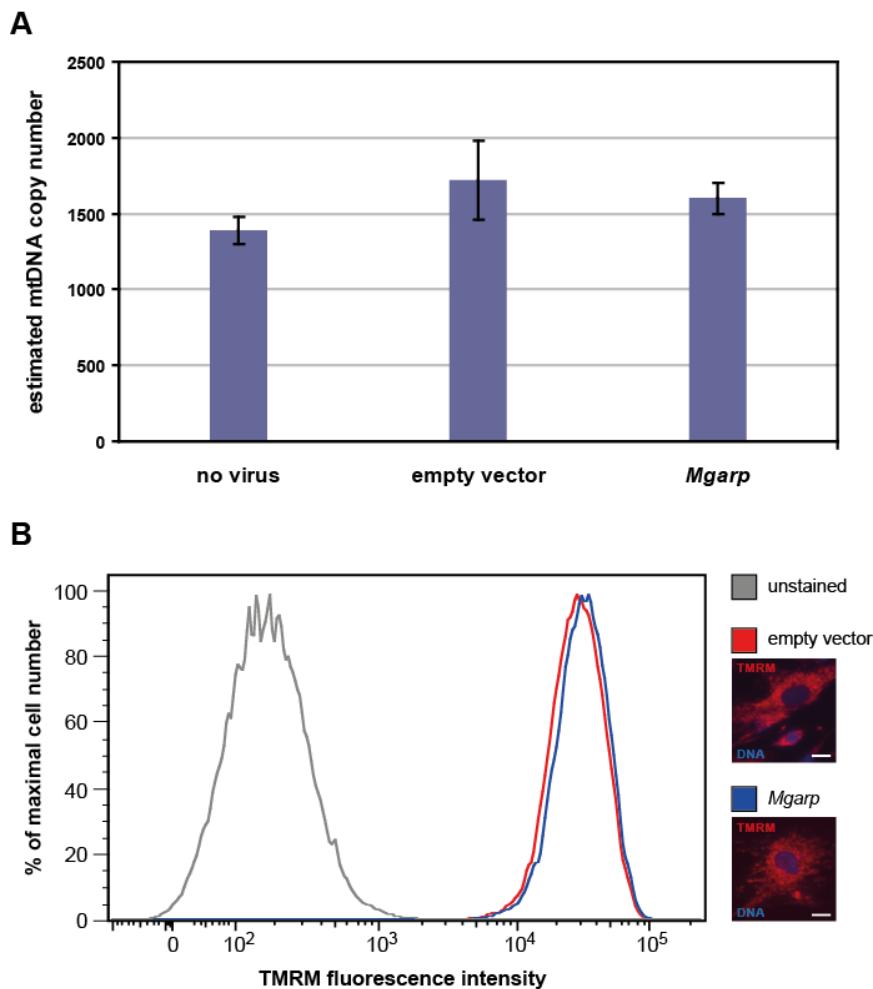


Figure S6, related to Figure 6. Mitochondria number and membrane potential upon overexpression of *Mgarp* in MEFs

(A) Mitochondrial DNA (mtDNA) copy number after 7 days of *Mgarp* overexpression assessed by qPCR on total cellular DNA. Absolute copy numbers were estimated by normalization to the two presumable copies of genomic *Actb* per diploid cell. Error bars correspond to the standard deviation of the mean (technical replicates, $n = 3$). (B) Quantification of mitochondrial tetramethylrhodamine methyl ester (TMRM) staining by flow cytometry 3 days after *Mgarp* overexpression. Single, living cells were pre-selected by gating for scatter characteristics and DAPI permeability. The histogram shows the normalized distribution of TMRM fluorescence intensity across the analyzed cell populations, indicating mitochondrial membrane potential and activity. Also shown are representative pictures of TMRM-stained mitochondria (red), overlayed with nuclear Hoechst staining (blue). Scale bars, 25 μ m. See also Table S5.

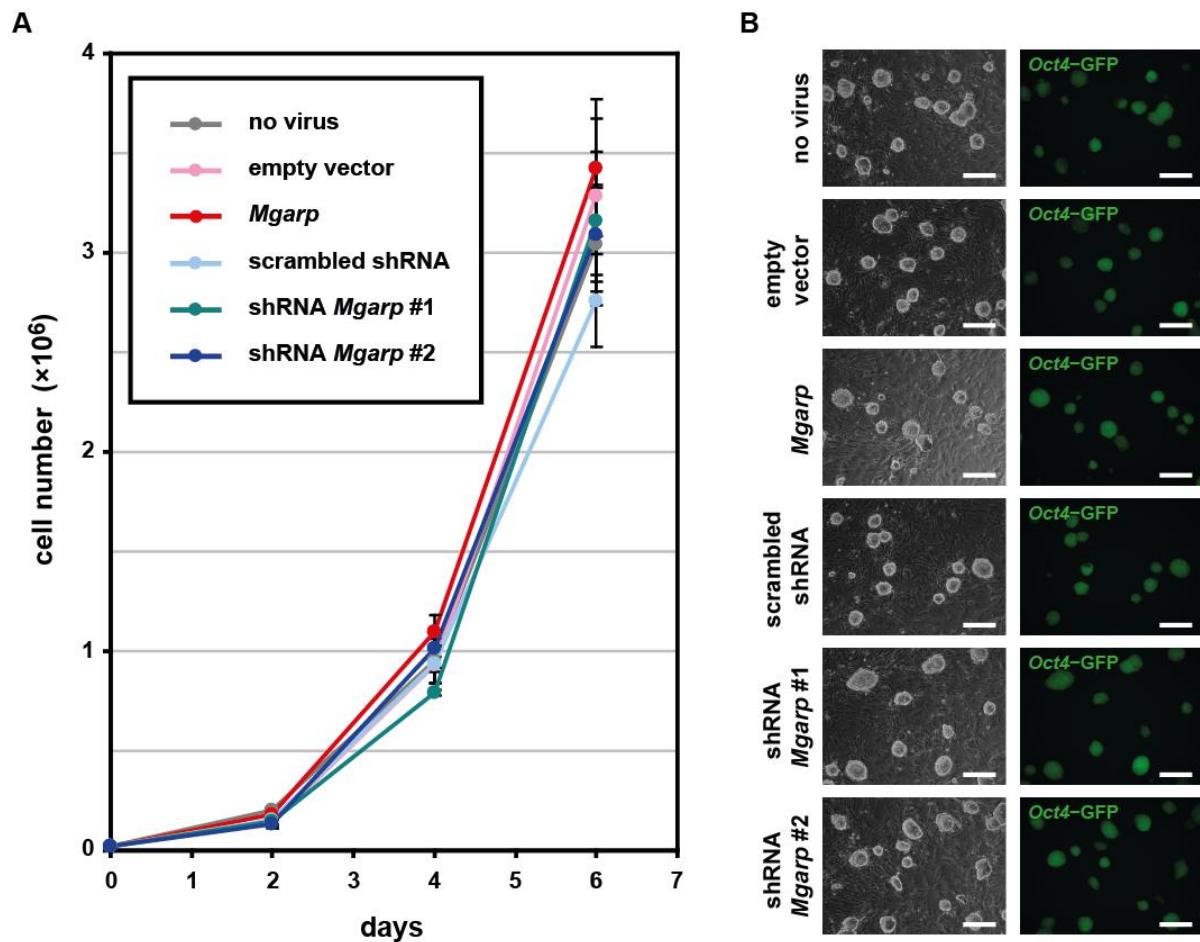


Figure S7, related to Figure 6. Proliferation rate, morphology, and *Oct4* expression in ESCs upon overexpression and knockdown of *Mgarp*

(A) 20,000 ESCs were seeded on day 0. Error bars correspond to the standard error of the mean (biological replicates, $n = 4$). (B) Phase-contrast and *Oct4*-GFP reporter fluorescence images of representative ESC cultures. Scale bars, 250 μ m.

Table S1, related to Figure 3. ESC-specific genes that were upregulated by OCT4 in the different somatic cell types

Regulation in cell type	ESC-specific probes
up in TO-MEFs	<i>Gca, Kndc1, Vgf, Mme, Tpd52l1, Zdhhc15, Tpd2l1, Vps41, Eml5, Stmn2, Flywch2, Chst8, Pthr1, St6glnac2, 4921528G01Rik, Tsc1, Ralgps2, Tek, Tfdp2, Isl1, Rassf7, Yipf2, 9430079M16Rik, Obfc1</i>
up in TO-NSCs	<i>Ryr1, Rnf125, Amigo2, Smtnl2, Mapt, Kndc1, Col9a2, Bmf, Zfp423, Clcn2, Mt2, Lgals4, Pacsin1, Zfp423, 4921528G01Rik, 1190005I06Rik, Syt9, Hr, Pnma2, Ralgps2, Vps41, Chst8, Arl5b, Mtmr14, LOC545238, Mpv17l</i>
up in TO-BMCs	Vgf

Probes present in more than one cell type are set in bold font.

Table S2, related to Figure 3. Enriched gene ontology (GO) terms of OCT4-regulated genes in TO-MEF cells and corresponding p-values after Benjamini-Hochberg correction for multiple hypothesis testing

regulation in cell type	GO identifier	category ^a	ontology term	p-value
up in TO-MEFs	GO:0043005	CC	neuron projection	2.15E-04
down in TO-MEFs	GO:0031012	CC	extracellular matrix	2.04E-09
down in TO-MEFs	GO:0005578	CC	proteinaceous extracellular matrix	2.54E-08
down in TO-MEFs	GO:0044421	CC	extracellular region part	2.98E-08
down in TO-MEFs	GO:0044420	CC	extracellular matrix part	1.28E-06
down in TO-MEFs	GO:0005515	MF	protein binding	7.48E-06
down in TO-MEFs	GO:0048513	BP	organ development	9.86E-06
down in TO-MEFs	GO:0048856	BP	anatomical structure development	2.77E-05
down in TO-MEFs	GO:0030198	BP	extracellular matrix organization	3.06E-05
down in TO-MEFs	GO:0007275	BP	multicellular organismal development	3.11E-05
down in TO-MEFs	GO:0043062	BP	extracellular structure organization	3.29E-05
down in TO-MEFs	GO:0048731	BP	system development	4.01E-05
down in TO-MEFs	GO:0032502	BP	developmental process	9.62E-05
down in TO-MEFs	GO:0009888	BP	tissue development	1.29E-04
down in TO-MEFs	GO:0048522	BP	positive regulation of cellular process	2.65E-04
down in TO-MEFs	GO:0009653	BP	anatomical structure morphogenesis	2.74E-04
down in TO-MEFs	GO:0001944	BP	vasculature development	2.75E-04
down in TO-MEFs	GO:0042127	BP	regulation of cell proliferation	4.02E-04
down in TO-MEFs	GO:0001568	BP	blood vessel development	4.81E-04
down in TO-MEFs	GO:0005576	CC	extracellular region	5.84E-04
down in TO-MEFs	GO:0005730	CC	nucleolus	7.22E-04
down in TO-MEFs	GO:0009987	BP	cellular process	8.24E-04

^aCC, cellular component; MF, molecular function; BP, biological process.

Terms that also appeared in other cell types are set in bold font.

Table S3, related to Figure 3. Enriched gene ontology (GO) terms of OCT4-regulated genes in TO-NSC cells and corresponding p-values after Benjamini-Hochberg correction for multiple hypothesis testing

regulation in cell type	GO identifier	category ^a	ontology term	p-value
down in TO-NSCs	GO:0044424	CC	intracellular part	4.63E-38
down in TO-NSCs	GO:0005622	CC	intracellular	5.74E-37
down in TO-NSCs	GO:0005634	CC	nucleus	3.32E-36
down in TO-NSCs	GO:0007049	BP	cell cycle	1.94E-35
down in TO-NSCs	GO:0043226	CC	organelle	1.23E-33
down in TO-NSCs	GO:0043229	CC	intracellular organelle	1.29E-33
down in TO-NSCs	GO:0005694	CC	chromosome	8.09E-32
down in TO-NSCs	GO:0043228	CC	non-membrane–bounded organelle	8.64E-31
down in TO-NSCs	GO:0043232	CC	intracellular non-membrane–bounded organelle	8.64E-31
down in TO-NSCs	GO:0043231	CC	intracellular membrane-bounded organelle	1.03E-30
down in TO-NSCs	GO:0043227	CC	membrane-bounded organelle	1.17E-30
down in TO-NSCs	GO:0044422	CC	organelle part	2.69E-30
down in TO-NSCs	GO:0044446	CC	intracellular organelle part	2.78E-30
down in TO-NSCs	GO:0022403	BP	cell cycle phase	6.61E-30
down in TO-NSCs	GO:0006259	BP	DNA metabolic process	3.72E-29
down in TO-NSCs	GO:0022402	BP	cell cycle process	3.96E-29
down in TO-NSCs	GO:0000278	BP	mitotic cell cycle	7.65E-29
down in TO-NSCs	GO:0009987	BP	cellular process	1.44E-27
down in TO-NSCs	GO:0000279	BP	M phase	2.93E-27
down in TO-NSCs	GO:0051301	BP	cell division	3.24E-27
down in TO-NSCs	GO:0044427	CC	chromosomal part	4.41E-26
down in TO-NSCs	GO:0000280	BP	nuclear division	3.78E-25
down in TO-NSCs	GO:0007067	BP	mitosis	3.78E-25
down in TO-NSCs	GO:0000087	BP	M phase of mitotic cell cycle	8.04E-25
down in TO-NSCs	GO:0048285	BP	organelle fission	1.69E-24
down in TO-NSCs	GO:0006260	BP	DNA replication	2.35E-23
down in TO-NSCs	GO:0000775	CC	chromosome, centromeric region	1.66E-20
down in TO-NSCs	GO:0044428	CC	nuclear part	3.40E-18
down in TO-NSCs	GO:0006139	BP	nucleobase, nucleoside, nucleotide, and nucleic acid metabolic process	3.79E-15
down in TO-NSCs	GO:0000793	CC	condensed chromosome	2.26E-14
down in TO-NSCs	GO:0044237	BP	cellular metabolic process	3.28E-14
down in TO-NSCs	GO:0006281	BP	DNA repair	7.65E-14
down in TO-NSCs	GO:0034641	BP	cellular nitrogen compound metabolic process	1.00E-13
down in TO-NSCs	GO:0006996	BP	organelle organization	2.70E-13
down in TO-NSCs	GO:0000776	CC	kinetochore	4.59E-13
down in TO-NSCs	GO:0006974	BP	response to DNA damage stimulus	8.42E-13
down in TO-NSCs	GO:0006807	BP	nitrogen compound metabolic process	1.06E-12
down in TO-NSCs	GO:0000779	CC	condensed chromosome, centromeric region	1.77E-12
down in TO-NSCs	GO:0005730	CC	nucleolus	1.82E-12
down in TO-NSCs	GO:0032991	CC	macromolecular complex	1.83E-12
down in TO-NSCs	GO:0000777	CC	condensed chromosome kinetochore	1.87E-12
down in TO-NSCs	GO:0031974	CC	membrane-enclosed lumen	1.91E-12
down in TO-NSCs	GO:0044238	BP	primary metabolic process	3.45E-11
down in TO-NSCs	GO:0005524	MF	ATP binding	8.84E-11
down in TO-NSCs	GO:0032559	MF	adenyl ribonucleotide binding	9.80E-11
down in TO-NSCs	GO:0044260	BP	cellular macromolecule metabolic process	1.03E-10
down in TO-NSCs	GO:0070013	CC	intracellular organelle lumen	1.16E-10
down in TO-NSCs	GO:0043233	CC	organelle lumen	1.33E-10
down in TO-NSCs	GO:0007059	BP	chromosome segregation	1.98E-10
down in TO-NSCs	GO:0030554	MF	adenyl nucleotide binding	3.11E-10
down in TO-NSCs	GO:0008152	BP	metabolic process	3.16E-10
down in TO-NSCs	GO:0001883	MF	purine nucleoside binding	4.28E-10
down in TO-NSCs	GO:0001882	MF	nucleoside binding	4.52E-10
down in TO-NSCs	GO:0031981	CC	nuclear lumen	6.72E-10
down in TO-NSCs	GO:0003824	MF	catalytic activity	1.66E-09
down in TO-NSCs	GO:0016043	BP	cellular component organization	1.96E-09

regulation in cell type	GO identifier	category ^a	ontology term	p-value
down in TO-NSCs	GO:0043234	CC	protein complex	1.97E-09
down in TO-NSCs	GO:0033554	BP	cellular response to stress	8.02E-09
down in TO-NSCs	GO:0032553	MF	ribonucleotide binding	1.37E-08
down in TO-NSCs	GO:0032555	MF	purine ribonucleotide binding	1.37E-08
down in TO-NSCs	GO:0017076	MF	purine nucleotide binding	3.66E-08
down in TO-NSCs	GO:0000166	MF	nucleotide binding	5.30E-08
down in TO-NSCs	GO:0043170	BP	macromolecule metabolic process	1.14E-07
down in TO-NSCs	GO:0006310	BP	DNA recombination	1.45E-07
down in TO-NSCs	GO:0005657	CC	replication fork	2.25E-07
down in TO-NSCs	GO:0022613	BP	ribonucleoprotein complex biogenesis	2.25E-07
down in TO-NSCs	GO:0051276	BP	chromosome organization	2.65E-07
down in TO-NSCs	GO:0006261	BP	DNA-dependent DNA replication	4.35E-07
down in TO-NSCs	GO:0015630	CC	microtubule cytoskeleton	4.64E-07
down in TO-NSCs	GO:0051716	BP	cellular response to stimulus	4.98E-07
down in TO-NSCs	GO:0005819	CC	spindle	6.05E-07
down in TO-NSCs	GO:0005635	CC	nuclear envelope	8.18E-07
down in TO-NSCs	GO:0034660	BP	ncRNA metabolic process	8.39E-07
down in TO-NSCs	GO:0005488	MF	binding	1.36E-06
down in TO-NSCs	GO:0006270	BP	DNA replication initiation	1.50E-06
down in TO-NSCs	GO:0042254	BP	ribosome biogenesis	3.35E-06
down in TO-NSCs	GO:0034621	BP	cellular macromolecular complex subunit organization	5.73E-06
down in TO-NSCs	GO:0032993	CC	protein-DNA complex	9.64E-06
down in TO-NSCs	GO:0005737	CC	cytoplasm	1.35E-05
down in TO-NSCs	GO:0009058	BP	biosynthetic process	1.37E-05
down in TO-NSCs	GO:0005643	CC	nuclear pore	1.81E-05
down in TO-NSCs	GO:0006323	BP	DNA packaging	1.91E-05
down in TO-NSCs	GO:0034470	BP	ncRNA processing	2.51E-05
down in TO-NSCs	GO:0006695	BP	cholesterol biosynthetic process	2.52E-05
down in TO-NSCs	GO:0003677	MF	DNA binding	2.84E-05
down in TO-NSCs	GO:0016126	BP	sterol biosynthetic process	3.26E-05
down in TO-NSCs	GO:0006364	BP	rRNA processing	5.03E-05
down in TO-NSCs	GO:0016072	BP	rRNA metabolic process	5.75E-05
down in TO-NSCs	GO:0044085	BP	cellular component biogenesis	5.75E-05
down in TO-NSCs	GO:0044430	CC	cytoskeletal part	7.35E-05
down in TO-NSCs	GO:0003676	MF	nucleic acid binding	9.50E-05
down in TO-NSCs	GO:0044249	BP	cellular biosynthetic process	1.19E-04
down in TO-NSCs	GO:0034622	BP	cellular macromolecular complex assembly	1.69E-04
down in TO-NSCs	GO:0046930	CC	pore complex	1.82E-04
down in TO-NSCs	GO:0016740	MF	transferase activity	1.86E-04
down in TO-NSCs	GO:0007017	BP	microtubule-based process	1.87E-04
down in TO-NSCs	GO:0006396	BP	RNA processing	2.29E-04
down in TO-NSCs	GO:0044454	CC	nuclear chromosome part	3.19E-04
down in TO-NSCs	GO:0043933	BP	macromolecular complex subunit organization	3.27E-04
down in TO-NSCs	GO:0012505	CC	endomembrane system	3.67E-04
down in TO-NSCs	GO:0016462	MF	pyrophosphatase activity	3.97E-04
down in TO-NSCs	GO:0016818	MF	hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides	3.98E-04
down in TO-NSCs	GO:0003887	MF	DNA-directed DNA polymerase activity	4.10E-04
down in TO-NSCs	GO:0009262	BP	deoxyribonucleotide metabolic process	4.52E-04
down in TO-NSCs	GO:0000228	CC	nuclear chromosome	5.10E-04
down in TO-NSCs	GO:0016817	MF	hydrolase activity, acting on acid anhydrides	5.34E-04
down in TO-NSCs	GO:0034061	MF	DNA polymerase activity	7.80E-04
down in TO-NSCs	GO:0031967	CC	organelle envelope	8.63E-04

regulation in cell type	GO identifier	category ^a	ontology term	p-value
down in TO-NSCs	GO:0031975	CC	envelope	8.89E-04
down in TO-NSCs	GO:0000785	CC	chromatin	8.90E-04
down in TO-NSCs	GO:0005856	CC	cytoskeleton	9.25E-04

^aCC, cellular component; MF, molecular function; BP, biological process.

Terms that also appeared in other cell types are set in bold font.

Table S4, related to Figure 3. Enriched gene ontology (GO) terms of OCT4-regulated genes in TO-BMC cells and corresponding p-values after Benjamini-Hochberg correction for multiple hypothesis testing

regulation in cell type	GO identifier	category ^a	ontology term	p-value
down in TO-BMCs	GO:0050896	BP	response to stimulus	2.48E-08
down in TO-BMCs	GO:0002376	BP	immune system process	6.16E-08
down in TO-BMCs	GO:0006955	BP	immune response	9.30E-08
down in TO-BMCs	GO:0009605	BP	response to external stimulus	1.09E-07
down in TO-BMCs	GO:0005576	CC	extracellular region	5.75E-07
down in TO-BMCs	GO:0006952	BP	defense response	8.35E-06
down in TO-BMCs	GO:0009611	BP	response to wounding	1.63E-05
down in TO-BMCs	GO:0006950	BP	response to stress	3.77E-05
down in TO-BMCs	GO:0009607	BP	response to biotic stimulus	7.70E-05
down in TO-BMCs	GO:0007599	BP	hemostasis	1.31E-04
down in TO-BMCs	GO:0051707	BP	response to other organism	1.43E-04
down in TO-BMCs	GO:0007596	BP	blood coagulation	1.45E-04
down in TO-BMCs	GO:0050817	BP	coagulation	1.45E-04
down in TO-BMCs	GO:0042060	BP	wound healing	2.69E-04
down in TO-BMCs	GO:0050878	BP	regulation of body fluid levels	5.15E-04

^aCC, cellular component; MF, molecular function; BP, biological process.

Terms that also appeared in other cell types are set in bold font.

Table S5, related to Figures 1, 2, 5, 6, 7, S5, and S6. Sequences of PCR primers

primer	sequence
<i>Oct4</i> qRT-PCR fw.	5'-GGC TAG AGA AGG ATG TGG TTC GAG-3'
<i>Oct4</i> qRT-PCR rev.	5'-CCT GGG AAA GGT GTC CCT GTA G-3'
<i>Parml</i> qRT-PCR fw.	5'-CAG TCA TCG CCG TAG TGT TGC-3'
<i>Parml</i> qRT-PCR rev.	5'-TCG TCC AGC AGC CTT CCA TA-3'
<i>Mgarp</i> qRT-PCR fw.	5'-AAA GAA CAA ACA AAG GCG GAG TTG-3'
<i>Mgarp</i> qRT-PCR rev.	5'-CAC ACT TGC TCG GCT TCT GC-3'
<i>Slc24a3</i> qRT-PCR fw.	5'-TGG TCC TCC ACG TGC TCT GT-3'
<i>Slc24a3</i> qRT-PCR rev.	5'-TCC AAG GAT GGG ACG AAG AAG T-3'
<i>Tmem53</i> qRT-PCR fw.	5'-AGG CTG CAG GGA CAA GAA CCT-3'
<i>Tmem53</i> qRT-PCR rev.	5'-GGG ATG CCC AAG GAC TCA GA-3'
<i>Adora2b</i> qRT-PCR fw.	5'-CGT CCC GCT CAG GTA TAA AGG TT-3'
<i>Adora2b</i> qRT-PCR rev.	5'-AGG CAA GGA CCC AGA GGA CA-3'
<i>Kank4</i> qRT-PCR fw.	5'-CAA CCT GGC TGA CCG AAG TG-3'
<i>Kank4</i> qRT-PCR rev.	5'-TTG ACA ATG GCG AAG TTG GAG T-3'
<i>Gap43</i> qRT-PCR fw.	5'-GCA GAA AGC AGC CAA GCT GA-3'
<i>Gap43</i> qRT-PCR rev.	5'-TCC TGT CGG GCA CTT TCC TT-3'
<i>Gadd45g</i> qRT-PCR fw.	5'-ACG AGT CCG CCA AAG TCC TG-3'
<i>Gadd45g</i> qRT-PCR rev.	5'-GCG CTA TGT CGC CCT CAT CT-3'
<i>Gapdh</i> qRT-PCR fw.	5'-CCA ATG TGT CCG TCG TGG AT-3'
<i>Gapdh</i> qRT-PCR rev.	5'-TGC CTG CTT CAC CAC CTT CT-3'
<i>Actb</i> qRT-PCR fw.	5'-ACT GCC GCA TCC TCT TCC TC-3'
<i>Actb</i> qRT-PCR rev.	5'-CCG CTC GTT GCC AAT AGT GA-3'
<i>Oct4</i> methylation 1 st fw.	5'-TTT GTT TTT TTA TTT ATT TAG GGG G-3'
<i>Oct4</i> methylation 1 st rev.	5'-ATC CCC AAT ACC TCT AAA CCT AAT C-3'
<i>Oct4</i> methylation 2 nd fw.	5'-GGG TTA GAG GTT AAG GTT AGA GGG-3'
<i>Oct4</i> methylation 2 nd rev.	5'-CCC CCA CCT AAT AAA AAT AAA AAA A-3'
<i>Nanog</i> methylation 1 st fw.	5'-TTT GTA GGT GGG ATT AAT TGT GAA-3'
<i>Nanog</i> methylation 1 st rev.	5'-AAA AAA TTT TAA ACA ACA ACC AAA AA-3'
<i>Nanog</i> methylation 2 nd fw.	5'-TTT GTA GGT GGG ATT AAT TGT GAA-3'
<i>Nanog</i> methylation 2 nd rev.	5'-AAA AAA ACA AAA CAC CAA CCA AAT-3'
GFP genotyping fw.	5'-GGA AAA GAA TTG GTA TCC AC-3'
GFP genotyping rev.	5'-GAT TAT AAC AGC TGG GTT GCC-3'
<i>Mgarp_a</i> ChIP fw.	5'-AGG CTT GTG GAC TCG AAG CCA GTG-3'
<i>Mgarp_a</i> ChIP rev.	5'-GCC TCT GTG TCT GTG TCT GCC TCC-3'
<i>Mgarp_b</i> ChIP fw.	5'-GCT CTA ACT CTG GTT GGT CTG ACG C-3'
<i>Mgarp_b</i> ChIP rev.	5'-TCT GTG AGT TTA AGG TCA GCC TTC TC-3'
<i>Mgarp_c</i> ChIP fw.	5'-GTC TCC AGC TTC CCG TTC TGG CAT-3'
<i>Mgarp_c</i> ChIP rev.	5'-ACC CAA ACA CAG TGC TCC TCC ACA-3'
<i>Mgarp_d</i> ChIP fw.	5'-TGG ATG TGA CAG GAA GCA TTT GCG-3'
<i>Mgarp_d</i> ChIP rev.	5'-ACA TTG AAA ATG GCT CCT TGG TGG T-3'
<i>Mgarp_e</i> ChIP fw.	5'-AGG TTT GGC CTC TCA CCG TAA GCA-3'
<i>Mgarp_e</i> ChIP rev.	5'-TGG AGA CCA GCA AGT CTG AGG ACC A-3'
<i>Mgarp_f</i> ChIP fw.	5'-GAG CAG AGA AAT CGT GAC CCG GCA-3'
<i>Mgarp_f</i> ChIP rev.	5'-ATG CGT GAT GTA TGC TCA GCC CGA-3'
<i>Mgarp_g</i> ChIP fw.	5'-GCC ATC GCC AGG GGG AAA CCT TAC-3'
<i>Mgarp_g</i> ChIP rev.	5'-GCA TTC CCA GGA AGA GGT AGC GGG-3'
<i>Mgarp_h</i> ChIP fw.	5'-CTC CCT CTG AGC CTG GGT TGC TTG-3'
<i>Mgarp_h</i> ChIP rev.	5'-CGG AGA TAC ATC GCC AGA TGC GCT-3'
<i>Mgarp_i</i> ChIP fw.	5'-GGG AAT GCG TGA GGA AAT GCG CTC-3'
<i>Mgarp_i</i> ChIP rev.	5'-ACA GAG AGG GTG GGC AGC TAG GAG-3'
<i>Mgarp_j</i> ChIP fw.	5'-GCC CCC TGT ACT CCC TTG AGT CCT-3'
<i>Mgarp_j</i> ChIP rev.	5'-GGA GGA GTG GGA GGC AGA GGA TGT-3'
<i>Mgarp_k</i> ChIP fw.	5'-GCC AGC CCT TTT TCT TTC TTT CTC A-3'
<i>Mgarp_k</i> ChIP rev.	5'-GCA GAA GGG CTC AGA TGT ATG GGT-3'
<i>Mgarp_l</i> ChIP fw.	5'-CTC CAG GAC CCA CGT AGT GGG AGA-3'
<i>Mgarp_l</i> ChIP rev.	5'-GGG CTG TTG GAA TCG CCT GGA TCA-3'
<i>Mgarp_m</i> ChIP fw.	5'-TGC CTT GCT TCC TAG CTC ATG CCA-3'
<i>Mgarp_m</i> ChIP rev.	5'-TGG AAT GCC AAC CAC ACT GGC CTT-3'
rDNA-28S ChIP fw.	5'-CTG GGT ATA GGG GCG AAA GAC-3'
rDNA-28S ChIP rev.	5'-GGC CCC AAG ACC TCT AAT CAT-3'
<i>Oct4</i> ChIP fw.	5'-GTT GAG AGT TCT GGG CAG ACG GCA-3'
<i>Oct4</i> ChIP rev.	5'-CCC AGG GCA GAG CTA TCA TGC ACC-3'

primer	sequence
<i>Cdh1</i> ChIP fw.	5'-CCA TGT CTC CGT GGG TCA GAG CAC-3'
<i>Cdh1</i> ChIP fw.	5'-TGT CTG TAG TTG GTG GCA TGG GGC-3'
mtDNA qPCR fw.	5'-ACA TTC CTA TGG ATC CGA GC-3'
mtDNA qPCR rev.	5'-GAT GAT GGC AAG GGT GAT AG-3'
<i>Actb</i> qPCR fw.	5'-CCC TAC AGT GCT GTG GGT TT-3'
<i>Actb</i> qPCR rev.	5'-GAG ACA TGC AAG GAG TGC AA-3'
sh <i>Mgrap</i> #1	5'-AGA CAC TGC TGT AAC GGA AGC TGA A-3'
sh <i>Mgrap</i> #2	5'-CAA AGC AAG TGA GAC GTA CAG AAC A-3'
shRNA control	5'-GTT CAG ATG TGC GGC GAG T-3'

fw., forward; rev., reverse.

Table S6, related to Figures 1, 2, and 7. Antibody information

antigen	host and clonality	clone / specification	manufacturer	dilution
OCT4	goat polyclonal	N19 sc-8628	Santa Cruz Biotechnology	1 : 1000
GAPDH	mouse monoclonal	AM4300	Ambion	1 : 10,000
NANOG	rabbit polyclonal	REC-RCAB0002P-F	Cosmo Bio	1 : 1000
SSEA-1	mouse monoclonal	MC-480	Millipore	1 : 100
TUBB3	mouse monoclonal	TUJ1 MMS-435P	Covance	1 : 1000
ACTA2	mouse monoclonal	1A4	Dako	1 : 100
SOX17	goat polyclonal	AF1924	R&D Systems	1 : 100
KLF4	goat polyclonal	AF3158	R&D Systems	1 : 1000

Supplemental References

Sabour, D., Araúzo-Bravo, M.J., Hübner, K., Ko, K., Greber, B., Gentile, L., Stehling, M., and Schöler, H.R. (2011). Identification of genes specific to mouse primordial germ cells through dynamic global gene expression. *Human molecular genetics* 20, 115-125.